

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: December 3, 2000, 10:15:26 ; Search time 10069.4 Seconds
(without alignments)
3236.486 Million cell updates/sec

Title: US-09-227-881-34
Perfect score: 5271
Sequence: 1 atcttgcagttacctc.....tcggcagtgagccagcaag 5271

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7189864 seqs, 3091403243 residues

Total number of hits satisfying chosen parameters: 14379728

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*
12: gb_est12:*
13: gb_est13:*
14: gb_est14:*
15: gb_est15:*
16: gb_est16:*
17: gb_est17:*
18: gb_est18:*
19: gb_est19:*
20: gb_est20:*
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37: gb_est37:*
38: gb_est38:*
39: gb_est39:*
40: gb_est40:*
41: em_estda:*
42: em_estfun:*
43: em_esthum1:*

44: em_esthum2:*
45: em_esthum3:*
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50: em_esthum8:*
51: em_esthum9:*
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87: em_estro13:*
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105: gb_gss14:*
106: gb_gss15:*
107: gb_gss16:*
108: gb_gss17:*
109: gb_gss18:*
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111: gb_gss20:*
112: gb_gss21:*
113: gb_gss22:*
114: gb_gss23:*
115: gb_gss24:*
116: em_gss5:*

117: em_gss6:*
118: em_gss7:*
119: em_gss8:*
120: em_gss9:*
121: em_gss10:*
122: em_gss11:*
123: em_gss12:*
124: em_gss13:*
125: em_gss14:*
126: em_gss15:*
127: em_gss16:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	180.8	3.4	660	88	AO057239	AO057239 CIT-HSP-2
2	179.8	3.4	539	96	AQ379787	AQ379787 RPC11-15
3	179	3.4	645	100	AQ36457	AQ36457 RPC1-11-4
4	179	3.4	678	96	AQ387027	AQ387027 RPC11-15
5	178.4	3.4	537	25	AM978041	AM978041 EST390150
6	177.6	3.4	516	89	AQ112451	AQ112451 CIT-HSP-2
7	177.4	3.4	577	91	AQ265389	AQ265389 CTBT-EI-
8	177.2	3.4	548	11	AI583291	AI583291 t55602.x
9	176.6	3.4	434	90	AO199435	AO199435 RPC11-58
10	176.6	3.4	531	25	AM979191	AM979191 EST391301
11	176	3.3	521	21	AM273360	AM273360 x138404.x
12	175.8	3.3	551	39	T53829	T53829 yb85d10.s1
13	175.8	3.3	559	91	AO283440	AO283440 RPC11-79
14	175.4	3.3	366	98	AQ474232	AQ474232 CTBT-EI-
15	175.2	3.3	711	97	AO415030	AO415030 RPT-11-2
16	175	3.3	368	19	AM069227	AM069227 CT4109.x
17	175	3.3	421	23	AM674631	AM674631 b41a11.x
18	175	3.3	447	24	AM820784	AM820784 RC2-ST030
19	175	3.3	454	12	AI634187	AI634187 t855a08.x
20	175	3.3	474	10	AI457313	AI457313 t173a05.x
21	175	3.3	527	11	AI523813	AI523813 t996a09.x
22	174.8	3.3	432	9	AI300818	AI300818 qn47c06.x
23	174.8	3.3	435	9	AI310992	AI310992 q095a06.x
24	174.6	3.3	424	10	AI431513	AI431513 t45f04.x
25	174.6	3.3	677	110	B66612	B66612 CIT-HSP-201
26	174.2	3.3	342	6	AA846923	AA846923 ce08d01.s
27	173.8	3.3	460	110	B15692	B15692 345N8.TP.CI
28	173.8	3.3	555	25	AM953220	AM953220 EST365290
29	173.6	3.3	368	21	AM270385	AM270385 xp74f06.x
30	173.6	3.3	374	37	F35684	F35684 HSPD32531.H
31	173.4	3.3	384	7	AA862029	AA862029 o14d604.s
32	173.4	3.3	427	5	AA550989	AA550989 n135d12.s
33	173.4	3.3	436	88	AO021084	AO021084 CIT-HSP-2
34	173.4	3.3	466	8	AI049955	AI049955 an38e01.x
35	173.4	3.3	642	110	B59854	B59854 CIT-HSP-345
36	173.2	3.3	836	102	AQ781145	AQ781145 HS_3122_A
37	173.2	3.3	433	10	AI355246	AI355246 gt74b06.x
38	173.2	3.3	430	13	AI859906	AI859906 wmc23c01.x
39	173.2	3.3	508	100	AO632598	AO632598 RPT-11-4
40	173.2	3.3	784	101	AQ738890	AQ738890 HS_5382_B
41	172.8	3.3	436	4	AA486819	AA486819 ab19c10.r
42	172.8	3.3	624	96	AQ373399	AQ373399 RPC11-15
43	172.6	3.3	397	10	AA937809	AA937809 nw89b02.s
44	172.4	3.3	397	10	AI417469	AI417469 th33n09.x
45	172.4	3.3	439	14	AI961983	AI961983 w41a12.x

ALIGNMENTS

RESULT 1
AO057239

LOCUS	AO057239	660 bp	DNA	GSS	30-JUL-1998
DEFINITION	CIT-HSP-2340D14.TF CIT-HSP Homo sapiens genomic clone 2340D14, DNA sequence.				
ACCESSION	AO057239				
VERSION	AO057239.1 GI:3353765				
KEYWORDS	GSS.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 660) Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Baas,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C. Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)				
TITLE	Unpublished (1998)				
JOURNAL	Other GSSs: CIT-HSP-2340D14.TF				
COMMENT	Contact: Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: mdadams@tigr.org Clones are available from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/cdb/humgen/bac_end_search/bac_end_search.html . Seq primer: M13 Reverse Class: BAC ends.				
FEATURES	Location/Qualifiers 1..660 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="2340D14" /clone_1lb="CIT-HSP" /sex="Male" /cell_type="Sperm" /note="Vector: pBelobAC11; Site_1: HindIII; Site_2: HindIII"				
BASE COUNT	116 a 188 c 150 g 206 t				
ORIGIN					
Query Match 3.4%; Score 180.8; DB 88; Length 660; Best Local Similarity 86.0%; Pred. No. 2.2e-21; Matches 215; Conservative 0; Mismatches 27; Indels 8; Gaps 1;					
QY	1321	acctgagctactgcaacacctgctccctccaggttcaagcaattctcttcaagctcc	1380		
DB	293	ATCTCAGCTCAGTCAACCTCTCTCCCGGTTCAAGCAATTCCTCTCAGCCTCC	352		
QY	1381	cgggtgctgagctcagagcg-----cagcccgagtaatttggatgttagta	1432		
DB	353	CAAGTAGCTGGAATTACAGCGCACACACACACGCCCGCTAATTTTGTATTTAGTA	412		
QY	1433	gagatggggttaccatataagctggctgcttgaactcctgacccctcaagtgatcca	1492		
DB	413	GAGATGGGTTTACACATGTTGGCAGGCGTGTGGAAGTCTGACCTGAGTGAATCA	472		
QY	1493	cccaactcagctcccaagtgctggatatacaggaatgaatcagcgccgccaagg	1552		
DB	473	CCACACCGCTGCTCCCAAGTGTGGGATTACAGCGCTGGCCACTGGCCAGCCTAAT	532		
QY	1553	gtcagtgatt 1562			
DB	533	TTTGTATT 542			
RESULT 2					
LOCUS	AO379787	539 bp	DNA	GSS	20-MAY-1999
DEFINITION	RPcII1-152C3.TJ RPc1-11 Homo sapiens genomic clone RPc1-11-152C3,				

RESULT 2
AQ379787/c 539 bp DNA GSS 20-MAY-1999
LOCUS AQ379787
DEFINITION RPC11-152c3.TF RPC1-11 Homo sapiens genomic clone RPC1-11-152c3,

DNA sequence.
ACCESSION AQ319787
VERSION AQ319787.1 GI:4350810
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 539)
AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
J.C.
TITLE Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
Map Building
JOURNAL Unpublished (1997)
COMMENT Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.bufileo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.bufileo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tldb/hungen/bac_end_search/bac_end_search.html
Seq primer: SP6
Class: BAC ends.

FEATURES
source Location/Qualifiers
1..539
/organism="Homo sapiens"
/db_xref="GDB:7558034"
/db_xref="taxon:9606"
/clone="RPCI-11-152C3"
/clone_11b="RPCI-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"
BASE COUNT 187 a 112 c 123 g 116 t 1 others
ORIGIN

Query Match 3.4%; Score 179.8; DB 96; Length 539;
Best Local Similarity 76.8%; Pred. No. 3.3e-21;
Matches 235; Conservative 0; Mismatches 63; Indels 8; Gaps 1;

OY 1280 aggggtgagggtctgtcttaccactacgtctgtcttaccactagctcactgaacc 1339
DB 327 AGAGTCTCCCTCTGTACACNAGGCTGAGTTCAGTGGCGGAGTCTGGCTCATCGAAC 268
OY 1340 tctgctccagggtcaagcaattctctctgtctcagctcccgcgtagctgggaactacag 1399
DB 267 TCTGCTCCCGGGTCAAGCAATTCCTGCTCCAGCTCCGAGTAGCTGGAGCACACAG 208
OY 1400 gc-----gaagcccgccgaatttctgtatgtttagtagagagaggggtttaccata 1451
DB 207 GATGTGCGCACCATACCCGGCTAATTTTGTATTATTAGTAGAAGGGGTTTCACCATC 148
OY 1452 ttagcccggtctgtcttgaactcctgaactcaggtgatccaccacactcagctcctctaa 1511
DB 147 TTGGCCAGGCTGGTCTTGAATCTCTGACCTCAGTGTATCCACAGCCTTGCCCTCTAA 88
OY 1512 gtgctggagattacaggaatgagtcacgcgcgcgcgaagggtcagtggttaagaa 1571
DB 87 GTGCTGGAGATTACAGAGTGAGTACACGCCGCGCTCAATCCCTTTTACAGTCTA 28
OY 1572 taactt 1577
DB 27 TGAATT 22

RESULT 3
AQ636457/c 645 bp DNA GSS 17-JUN-1999
LOCUS RPCI-11-465121.TV RPCI-11 Homo sapiens genomic clone RPCI-11-465121
DEFINITION 'DNA sequence.
ACCESSION AQ636457
VERSION AQ636457.1 GI:5099092
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 645)
AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
J.C.
TITLE Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
Map Building
JOURNAL Unpublished (1997)
COMMENT Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.bufileo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.bufileo.edu/ordering) or from
Research genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tldb/hungen/bac_end_search/bac_end_search.html.
Seq primer: SP6
Class: BAC ends.

FEATURES
source Location/Qualifiers
1..645
/organism="Homo sapiens"
/db_xref="GDB:7678388"
/db_xref="taxon:9606"
/clone="RPCI-11-465121"
/clone_11b="RPCI-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"
BASE COUNT 214 a 118 c 139 g 174 t
ORIGIN

Query Match 3.4%; Score 179; DB 100; Length 645;
Best Local Similarity 88.2%; Pred. No. 4.5e-21;
Matches 209; Conservative 0; Mismatches 20; Indels 8; Gaps 1;

OY 1322 cctgagctacgtgcaactctctcccaaggttcaagcaattctctgtctcagctccc 1381
DB 248 CTTCACACTCAGTCAACACCTCTCTCCCTCCAGTTCAGTAATCTCTCTCAGCTCC 189
OY 1382 ggttagctggagctcagcg-----caagcccggttaattttttagttagtag 1433
DB 188 GATAGCTGTGGATTTACAGCGGTGTGTACACCGCCAGCTAATTTTGTATTATTAGTAG 129
OY 1434 agatggggtttacacatataaccccgctgctgtgaactcctgaactcaggtgattcacac 1493
DB 128 AGATGGGATTTACACCATGTGTGGCAGAGCGTGTCTCGACTCTGACCTCAAGTATCTGC 69
OY 1494 ccaactcagcctctaagtgctgggattacaggaatgagtcacgcgcgcgcgcgcacaa 1550
DB 68 CCACCTCAGCCTCCCAAAAGTGTGGATTACAGGATGAGCACCGCCGCCGCCAA 12

RESULT 4
AQ387027/c 678 bp DNA GSS 21-MAY-1999
LOCUS AQ387027
DEFINITION RPCI11-153C12.TV RPCI-11 Homo sapiens genomic clone RPCI-11-153C12,

ACCESSION	DNA sequence.	
VERSION	AQ387027	
KEYWORDS	GI:4358050	
SOURCE	GSS.	
ORGANISM	human.	
REFERENCE	Homo sapiens	
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
TITLE	1 (bases 1 to 678)	
JOURNAL	Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter,J.C.	
COMMENT	Use of BAC End Sequences from Library RPC1-11 for Sequence-Ready Map Building Unpublished (1997) Other GSSs: RPC11-153C12, TV Contact: Shaying Zhao, William Nierman, Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850 Tel: 301 838 0200 Fax: 301 838 0208 Email: hbe@tigr.org Clones are derived from the human BAC library RPC1-11. For BAC library availability, please contact Pieter de Jong (pieter@tigr.org, med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search.html Seq primer: SP6 Class: BAC ends.	
FEATURES	Location/Qualifiers	
source	1..678	
	/organism="Homo sapiens"	
	/db_xref="GDB:7558427"	
	/db_xref="taxon:9606"	
	/clone="RPC1-11-153C12"	
	/clone_11b="RPC1-11"	
	/sex="Male"	
	/cell_type="Lymphocytes"	
	/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; RPC11 Human Male BAC Library"	
BASE COUNT	210 a 151 c 171 g 146 t	
ORIGIN		
Query Match	3.4%; Score 179; DB 96; Length 678;	
Best Local Similarity	77.4%; Pred. No. 4.4e-21;	
Matches 233; Conservative	0; Mismatches 60; Indels 8; Gaps 1.	
OY 1274	tcctgtagggtaggggtctgtctctaacaccacacgttagtctctacacctagctact 1333	
Db 364	TCACGACAGAGTCTTCTCTCTGTCGTCAGGCTGGAAGCAATGGACAGATCTGGCGCACT 305	
OY 1334	gcaacctctgctcccaaggttcaagaacattctctgtctcaagctcccgcgtagctgga 1393	
Db 304	GCAACCTCCGCTCCACAGTTCAACCAATTCCTGCGCTCCACCTCCCATGTAGCTGGCA 245	
OY 1394	ctacagggc-----gcaagccggcgcaattttgtatgtttagtagagatggaggttc 1445	
Db 244	TTACAGGCAACCCACACCACTGCGCGGCTAATTTTATTTATTTAGTAGAGATGGGCTTC 185	
OY 1446	accatatatgaccggcgtgtctctgaactctctacctcagtgatcatcaccacctcagct 1505	
Db 184	ACCAAGTGGCCAGGCTGGTCTCGAAGCTCTGACCTCAGATGATCGCCGCGCTTAGCCT 125	
OY 1506	cctaagatgctggattatcagagcatgagtcaaccggcccgcccaagggatcagtgttaat 1565	
Db 124	CCCAAAAGTGCTGGGATTCACAGCGCTGAGCCACCGCGCGCTTATTTATTTATTTAG 65	
OY 1566	a 1566	
Db 64	A 64	

[illegible]

KEYWORDS	GSS.
SOURCE	human.
ORGANISM	human sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
TITLE	Use of a random human BAC End Sequence Database for Sequence-Ready Map Building
JOURNAL	Unpublished (1998)
COMMENT	Other_GSSs: CIT-HSP-2372C9, TR Contact: Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: mdadams@tigr.org Clones are available from Research Genetics (Info@resgen.com). BAC end search page: http://www.tigr.org/tcdb/hungen/bac_end_search/bac_end_search.html . Seq primer: M13-21 Class: BAC ends.
FEATURES	Location/Qualifiers
SOURCE	1..516 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="2372C9" /clone_11b="CIT-HSP" /sex="Male" /cell-type="Sperm" /note="Vector: pBelobAC11; Site_1: HindIII; Site_2: HindIII"
BASE COUNT	87 a 145 c 118 g 166 t
ORIGIN	
Query Match	3.4%; Score 177.6; DB 89; Length 516;
Best Local Similarity	85.2%; Pred. No. 8e-21;
Matches 213; Conservative	0; Mismatches 29; Indels 8; Gaps 1
Oy	1321 accctgaagctactgtcaacctctgtcctccagggtcaagaatctctctcgaagctcc 1380
Db	255 ATCTCAGCTCATCTGCACACTCTGCTCCCGGGTTCAAGCGATTCTCTCTCAGCCTCC 314
Oy	1381 cgcgtcagctcgggaactcaagcg-----caagcccggtctaattttgatgttaagta 1432
Db	315 CAAGTAGCTGGGATTAACAGCGCACACACACACGCCCGCTTAATTTTGTATTTTAAAGTA 374
Oy	1433 ggaatgggggttcacacattagaccggctgtgtctgtgaactctctgaagctcaagtga 1492
Db	375 GAGATGGGGTTTCACCATTTTGCCACGCGCTGCTCTGAACTCTGACTTAAGTGATCCA 434
Oy	1493 ccacactcagcctctcctaagaatgtcgggaattacagaagcagtaagtcaccgcgcgcgcaaga 1552
Db	435 CCCACCTTGCGCTCCCAAGTGCTGGGATTAACAGCGCTGGGCACATGCGCCAGCCTAAT 494
Oy	1553 gtcaagtgttt 1562
Db	495 TTTTGCAATT 504
RESULT 7	
LOCUS	AO265389 577 bp DNA GSS 27-OCT-1998
DEFINITION	CITBI-21-2509010.TF CITBI-EI Homo sapiens genomic clone 2509010, DNA sequence.
ACCESSION	AO265389
VERSION	AO265389.1 GI:3793589
KEYWORDS	GSS.
SOURCE	human.

ORGANISM	Homo sapiens			
REFERENCE	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:			
AUTHORS	Mammalia: Euthera: Primates: Catarrhini: Homnidae: Homo.			
	1 (bases 1 to 577)			
	Adams,M.D., Rounsley,S.D., Zhao,S., Baas,S., Linher,K., Golden,K.,			
	Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and			
	Venter,J.C.			
TITLE	Use of a random human BAC End Sequence Database for Sequence-Ready			
JOURNAL	Map Building			
COMMENT	Unpublished (1998)			
	Other_GSSS: C17B1-E1-2509010.TR			
	Contact: Mark Adams			
	The Institute of Eukaryotic Genomics			
	9712 Medical Center Dr., Rockville, MD 20850, USA			
	Tel: 301 838 0200			
	Fax: 301 838 0208			
	Email: mdadams@tigr.org			
	Clones are available from Research Genetics (info@resgen.com). BAC			
	end search page:			
	http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.			
	Seq primer: M13-21			
	Class: BAC ends.			
FEATURES	Location/Qualifiers			
source	1..577			
	/organism="Homo sapiens"			
	/db_xref="taxon:9606"			
	/clone="2509010"			
	/clone_11b="C17B1-E1"			
	/sex="male"			
	/cell_type="sperm"			
	/note="Vector: pBeloBAC11, Site_1: EcoRI, Site_2: EcoRI;			
	Caltech Human BAC Library D			
BASE COUNT	167 a 127 c 137 g 146 t			
ORIGIN				
Query Match	3.4%; Score 177.4; DB 91; Length 577;			
Best Local Similarity	75.1%; Pred. No. 8.5e-21;			
Matches 238; Conservative	0; Mismatches 71; Indels 8; Gaps 1			
Oy	1321	accctgaagctcaatgaacctctgcctccaggcttaagaacatctctcctcgaagctcc	1380	
Db	368	ATCTGGGCTCACTGCAACCTCTGCTCCAGGTTCAAGATTTCTCTGCTCAAGCTTC	309	
Oy	1381	cgcgtgaagcttgagactacagagc-----gcacgcccggcctaatttttgatgtagta	1432	
Db	308	CGAGTAATCTAGAGACTACAGCGCACCGGCCACAGAGCTGGCTAATTTTGTATTTTAGTA	249	
Oy	1433	gagatgggggttcaccacataatgacccggcgtggtcttgaacctcgaagtgatgcca	1492	
Db	248	GAGAGCGGGTTTCACCAATGTTGTGTCAGGCTGCTTGAATCTCTGACCTCAGGCGATCCA	189	
Oy	1493	cccactcgaagcctctcctaagtgcttggtttaaggcatgacgacgagccggcgcaag	1552	
Db	188	CCCGCTTGGCCTCCCAAGTGCTGGGATTAAGCATGAGCCACTGCAAGCCACCA	129	
Oy	1553	gtcagtggttaataaggaataaacttgaatggtttactaacaacagaggaacagacaaa	1612	
Db	128	GATTAATTTTGTAAATCTAGACTGAGAGTCATGGACACACTCCTCAGCAGCAAGGAGAA	69	
Oy	1613	agctgtgataaattcag 1629		
Db	68	AGTAATACTGATGAG 52		
RESULT 8				
LOCUS	A1583291			
DEFINITION	A1583291 548 bp mRNA EST 14-DEC-1999			
	ttctggagc2.x1 NC1_CGAP_HSC4 Homo sapiens cDNA clone IMAGE:2244818 3'			
	similar to FR:Q13538 Q13538 ORF2: FUNCTION UNKNOWN. contains Alu			
	repetitive element, mRNA sequence.			
ACCESSION	A1583291			

VERSION	AT583291.1	GI:456198
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.	
TITLE	1 (bases 1 to 548)	
JOURNAL	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .	
COMMENT	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	
	Tumor Gene Index	
	Unpublished (1997)	
	Contact: Robert Strausberg, Ph.D.	
	Tel.: (301) 496-1550	
	Email: Robert.Strausberg@nih.gov	
	Tissue Procurement: Herbert Morse, M.D., Michael R. Emmert-Buck,	
	M.D., Ph.D.	
	cDNA Library Preparation: David B. Kitzman, Ph.D.	
	cDNA Library Arrayed by: Greg Lennon, Ph.D.	
	DNA Sequencing by: Washington University Genome Sequencing Center	
	Clone distribution: NCI-CGAP clone distribution information can be	
	found through the I.M.A.G.E. Consortium/LLNL at:	
	www-bio.llnl.gov/bbrp/image/image.html	
	Insert Length: 664	Std Error: 0.00
	Seq primer: ~400P from Gibco	
	High quality sequence stop: 464	
	POLYA-NO.	

FEATURES	SOURCE
location/Qualifiers	
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/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="IMAGE:2244818"	
/clone_lib="NCI CGAP_HSC4"	
/tissue_type="CD34+, CD38- from normal bone marrow donor"	
/lab_host="DH10B"	
/note="Organ: bone marrow; Vector: pAMP1; mRNA made from lymphoid tissue; cDNA made by oligo-dT priming. Directionally cloned. Size-selected on agarose gel, average insert size 500 bp. Primary library, non-amplified. cDNA library preparation: David B. Kitzman, Ph.D. Reference: Kitzman et al. (1996) Cancer Research 56:5380-5383."	
BASE COUNT	150 a 136 c 129 g 133 t
ORIGIN	

Query Match	3.4%	Score 177.2	DB 11	Length 548
Best Local Similarity	78.8%	Pred. No. 9,3e-21		
Matches 227	Conservative 0	Mismatches 53	Indels 8	Gaps 1
Qy 1277	gtgagagtgagaggtcttggtgtctaacaccctactatgtctctcaacacgtgagctactgtca			1336
Db 546	GAGGAGAGCTTTGATGTATGTGTGCTCAGGCTTGAGATGAGTGGCATGTATCTTGCTCTCACTGCA			487
Qy 1337	aacctctgctccccaaggtctcaagaacattctctctgtctcagagcctcccgctgagcttggaacta			1396
Db 486	ACCTCCGCTCTCAGAGGTTCACGACATTTCTCTGCTCCAGCCTCTCTGAGACGCTGAGACTA			427
Qy 1397	caaggg-----caagcccggtccaaatttttgatattgtatgtatgaatagataggggtttcaac			1448
Db 426	CAGCGGCCGCCACACACGCTGTGCAATTTTGTATTTTAACTAAGAGAGGGGCTTTCACC			367
Qy 1449	atatattgacccggctgtgtcttgaacctctgaacctcaagtgatcatccaccacactcagctcct			1508
Db 366	ATGTGTGGCCAGGCTGTGTGTGNAACCTCTGACCTCAGGTATATCCACCAACTTGTGCTGCC			307
Qy 1509	aaagtctgtggatctacaaggcatagatctacacgcgcgcgcgcgaagggtca			1556
Db 306	AAAGTCTGTGGATTCAGGCATGAGACCAACCGTGCACAGCCCAAGATTTA			259

RESULT	9			
AO199435/c				
LOCUS	AO199435	434 bp	DNA	GSS
				20-APR-1999

DEFINITION	RPc11-58F5..TJ RPc1-11 Homo sapiens genomic clone RPc1-11-58F5, DNA sequence.
ACCESSION	AO199435
VERSION	AO199435.1 GI:3611634
KEYWORDS	GSS.

SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 434)
AUTHORS	Adams,M.D., Rounsley,S.D., Zhao,S., Bess,S., Linher,K., Golden,K. Berry,K., Granger,D., Suh,E., Mible,C., de Jong,P. and Venter,J.C
TITLE	Use of human BAC End Sequences for Sequence-Ready Map Building
JOURNAL	unpublished (1998)
COMMENT	Other-GSSs: RPII1-58F5..TK

Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel.: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@tigr.org, med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering/>) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tldb/humgen/Bac_end_search/Bac_end_search.html
Class: BAC ends.

```

FEATURES
SOURCE
Location/Qualifiers
1. .434
/organism="Homo sapiens"
/db_xref="GDB:7522012"
/db_xref="taxon:9606"
/clone="RPC1-11-58P5"
/clone_11b="RPC1-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
RPC11 Human Male BAC Library"
BASE COUNT
118 a 108 c 114 g 94 t
ORIGIN

```

Query Match	3.4%	Score 176.6	DB 90	Length 434
Best Local Similarity	77.4%	Pred. No. 1.2e-20		
Matches 230	Conservative	0	Matches 59	Indels 8
				Gaps 1
Oy 1252	tgtgtcctaaccctaccctcgtatgctctacactgagctacatgcgaacctctgctccag	1351		
Db 427	tgtcactcaggtgagtgacagtgacatggcagcatcttgacctctctgcacacctctgctctgg	368		
Oy 1352	gttcaagcaatctctctgtctcagccctccgcgctagctggaactaaga	1403		
Db 367	gttcaagcaatctctctgtctcagccctcccaagtgatgacgtttacagcaccggccacac	308		
Oy 1404	acgcgcgcgctaattcttgatcttagtagaagatgagggttccaccatactagccgcgctg	1463		
Db 307	atgcccgctaatgttttggatgttttagtagacagatgggggtttcactatgttgccctggccta	248		
Oy 1464	gtcttgaacctctgaacctcaagtgatgccaccacctcagccctcctaagtgcttgatata	1523		
Db 247	gmcctgaactccggagctcagctgactgattccacctgcttgccctctgaagctctgggattta	188		
Oy 1524	cagcatcgaatcaccgcgcgcgcgcgaagggtcattgcttataaaggaataacttgaa	1580		
Db 187	cagtggtatgctaccgtcccgccagcagagatgtgggttttatccagaaagatctgaa	131		

RESULT	10
LOCUS	AW979191
DEFINITION	AW979191 591 bp mRNA EST
	EST391301 MAGE resequences, MAGEP Homo sapiens CDNA, mRNA sequence 02-JUN-2000

ACCESSION	AW979191
VERSION	AW979191.1
KEYWORDS	GI:8170478
SOURCE	human.
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE	1 (bases 1 to 591)
AUTHORS	'Hedde,P., Qi,R., Abernathy,K., Dharp,S., Gaspard,R., Gay,C., Holt,I.E., Saeed,A.I., Sharov,Y., Lee,N.H., Yeatman,T.J. and Quackenbush,J.'
TITLE	Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray
JOURNAL	Unpublished (2000)
COMMENT	Contact: John Quackenbush The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 3528 Fax: 301 838 0208 Email: johnqu@tigr.org Plate: 403 Seq primer: Forward. Location/Qualifiers 1..591 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_lib="MAGE resequences, MAGP" /note="Vector: pBluescriptSkm"
BASE COUNT	154 a 152 c 126 g 159 t
ORIGIN	
Query Match	3.4%; Score 176.6; DB 25; Length 591; Best Local Similarity 71.9%; Pred. No. 1.2e-20; Matches 248; Conservative 0; Mismatches 89; Indels 8; Gaps 1
Oy	1281 gggtgagggctcgtgtcttaacacctcccgtagtcctaacacttgagccactgaacacct 1340
Db	132 GAGCTTGTCTGTCATCCAGCGCTGAAGTGCACTGGCACATCTCGCATCCTGCACACT 191
Oy	1341 cgagctccaggattcaagaatctccgtctcagcctcccgcgtagctgagactaagg 1400
Db	192 CCACCTCCCAGGTTCAAGCAATTCTCTGTCTAAGCTCTTAAGTAGCTGGAGCTAGAAG 251
Oy	1401 cgcacg-----ccgcgctaatttttgtatgttagtagagaatggggtttaccatat 1452
Db	252 GGCGCGCCACCAATACCAGACTAATTTTTCATATTTTAGTAGAGATGGGGTTCCACCATAT 311
Oy	1453 tagccgcgctgtcttgaactcctgaactcgaagtatgccaccacactcgaacctccaag 1512
Db	312 TGGTCAGGCTGTGCTTGAACCTCTGACCTCAGGTGATCCACCGCTTGGCTCCCAAAG 371
Oy	1513 tgctgagattacaaggaatgagtcacgcgcgcgcgcaagggttcagctgtttaataagaat 1572
Db	372 TGCTGGGATGACAGGGCTGAGCCACTGCCGCCACCAAGTTCTGGAATTTTAAGCCA 431
Oy	1573 aaactgaatggttactaaaccaacagggaaacagacaaaagctg 1617
Db	432 AATATAATCTATTAACTCACTCAATGCACTTACTCAACAAGATG 476
RESULT 11	
LOCUS	AW273360 521 bp mRNA EST 03-JAN-2000
DEFINITION	xr38a04.x1 NCI_CGP_U14 HOMO SAPIENS CDNA clone IMAGE:2762382 3'
ACCESSION	similar to contains Alu repetitive element;contains L1.t2 L1 L1
VERSION	repetitive element ; mRNA sequence.
KEYWORDS	AM273360 GI:6660390
SOURCE	EST.
ORGANISM	human.
	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS 1 (bases 1 to 521)
TITLE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLW at:
www.bio.linnl.gov/bdrip/image/image.html

FEATURES
Source
Possible reversed clone: polyA not found
Seq primer: -40up from Gldco
High quality sequence stop: 411.
Location/Qualifiers
1..521
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2762382"
/clone_lib="NCI-CGAP_Ut4"
/tissue_type="serous papillary carcinoma, high grade, 2
pooled tumors"
/lab_host="DH10B"
/note="Organ: uterus; Vector: PCMV-SPORE; Site:1: SalI;
Site:2: NotI. Cloned unidirectionally. Primer: Oligo dT,
Average Insert size 1.48 kb. Life Technologies catalog #:
11542-016"

BASE COUNT 115 a 131 c 108 g 167 t
ORIGIN

Query Match 3.3%; Score 176; DB 21; Length 521;
Best Local Similarity 80.7%; Pred. No. 1.5e-20;
Matches 221; Conservative 0; Mismatches 45; Indels 8; Gaps 1;

OY 1321 accctaagctcatgtaaacactgcgtcccaaggttaaagaatttcctgctcaagctcc 1380
DB 56 ACTCTGGCCACTGCACACTGTGCTCCCAAGTTCAACGATTCCTGCTCAGCCTCC 115
OY 1381 ccgcagtacgggaaccacagcg-----cacgccgacataatcttgatctgtagta 1432
DB 116 TAGATAGCACGAGATTACAGTGCCGCCACACACCACCAAGTAATTTTGTATTTTAGA 175
OY 1433 gagatgagggttacacatatagcccgcgtggtcttgtaacctcgaacctcaagtgatcca 1492
DB 176 GAGATGGGGTTTCACTAATGTTGGCCAGCGCTAGTCTTGTACTGACCTCAGCATGATCCA 235
OY 1493 cccacctcagcctcttaaagtgcctggatltaaaggcatgagtcacccggccccggccaagg 1552
DB 236 CCCGGCTCAGCTCCCAAGAAGTCTGGGATTAAGGACATGACACGCCCTGGCCTTTC 295
OY 1553 gtccagtgttaataaggaataacttgaatgttt 1586
DB 296 CTGACTTTTAACTGATCACCATTCTAACGTGAT 329

RESULT 12
LOCUS T53829 551 bp mRNA EST 06-FEB-1995
DEFINITION yb58dl0.s1 Stratusgene liver (9937224) Homo sapiens cDNA clone
sequence.
ACCESSION T53829
VERSION T53829.1 GI:655690
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 551)
AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chapell, B.,
Chissole, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins,
M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore,
B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevisan, E.,
Underwood, K., Wohlmann, P., Waterston, R., Wilson, R., and Watra, M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
JOURNAL MEDLINE
97044478
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
Insert Size: 760
High quality sequence stops: 380 Source: IMAGE Consortium, LNL This
clone is available royalty-free through LNL; contact the IMAGE
Consortium (info@image.lnl.gov) for further information.
Insert Length: 760 Std Error: 0.00
Seq primer: -21m13
High quality sequence stop: 380.
Location/Qualifiers
1..551
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/db_xref="taxon:9606"
/clone="IMAGE:77971"
/clone_1lb="Stratagene Liver (#937224)"
/sex="male"
/dev_stage="49 years old"
/lab_host="SOLR cells (kanamycin resistant)"
/note="Organ: liver; Vector: pBluescript SK; Site_1: EcoRI
Site_2: XhoI; Cloned unidirectionally. Primer: Oligo
dT. Hepatectomy from normal male caucasian. Average insert
size: 1.1 kb. Uni-ZAP XR Vector: -5' adaptor sequence: 5'
GAATTCGGCAGAG 3' -5' adaptor sequence: 5'
CTCGAGTTTCTTTTCTTPT 3'".
BASE COUNT 119 a 134 c 127 g 163 t 8 others
ORIGIN

Query Match 3.3%; Score 176; DB 39; Length 551;
Best Local Similarity 80.7%; Pred. No. 1.5e-20;
Matches 221; Conservative 0; Mismatches 45; Indels 8; Gaps 1;

QY 1321 accgaagctactcaacacctgctccaggtcagaacattctctgtctagctcc 1380
DB 47 ATCTCGGCTACTCAACCTCTGCTCCAGATTCAAGCGATTCTCTGCTCAGCTCC 106
QY 1381 cgcgtacgtggtacacagcg-----cagcccgctaatcttctgattagta 1432
DB 107 TGACTACCAAGATTACAGTCCCGCCACACACCCAGCTAATTTTGTATTAGTA 166
QY 1433 gagaagggtttccacatattagccggtggtctgtaactcctgacctgaagtatca 1492
DB 167 GAGATGGGTTTACATATGTTGGCCAGCTAGTCTTGTACTCTGACCTCAGTGATCA 226
QY 1493 cccacccacacccctctaaagtctgggatacagagctaggtacccgcccagcgaag 1552
DB 227 CCGGCTCAGCCTCCCAAAGTGGGATTACAGACATGAGTCAACCCCTGGCCCTTC 286
QY 1553 gtccagtgcttaataagaataactgaatgttt 1586
DB 287 CTGACTTTTATGATGATCACCATTCTAATGATAT 320

RESULT 13
AQ283440

LOCUS AQ283440 589 bp DNA GSS 27-APR-1999
DEFINITION RPI11-7965.TJ RPI1-11 Homo sapiens genomic clone RPI1-11-7965, DNA
sequence.
ACCESSION AQ283440
VERSION AQ283440.1 GI:3908257
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 589)
AUTHORS Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.,
Berry, K., Granger, D., Suh, E., Mible, C., de Jong, P., and Venter, J.C.
Use of human BAC end sequences for Sequence-Ready Map Building
Unpublished (1998).
JOURNAL Other-GSS: RPI11-7965.TV
COMMENT Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
912 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are derived from the human BAC library RPI1-11. For BAC
library availability, please contact Plier de Jong
(plierdejong.med.buhalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buhalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/cdb/humgen/bac_end_search/bac_end_search.html
Seq primer: SP6
Class: BAC ends.
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="GDB:7530100"
/db_xref="taxon:9606"
/clone="RPI1-11-7965"
/clone_1lb="RPI1-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
RPI11 Human Male Library"
BASE COUNT 146 a 126 c 136 g 181 t
ORIGIN

Query Match 3.3%; Score 175.8; DB 91; Length 589;
Best Local Similarity 75.7%; Pred. No. 1.6e-20;
Matches 234; Conservative 0; Mismatches 67; Indels 8; Gaps 1;

QY 1280 aggtgaaggtctggtcttaacacctagctgtgctctacacctgagctcactgaacc 1339
DB 105 AGAGTCTTGCTCTGTGCCCCAGCTGAGTACAGTGTGAGTGTACCTACATGCCAAC 164
QY 1340 tctgctcccaaggttaagaacattctctgctcagaacctcccgtagctggaactaga 1399
DB 165 TCGACTCCTCGGTTCAAGAAATTCTCTGTCTTACGCCGCCAGTAGTGGGATTACAG 224
QY 1400 ggc-----cagcccgctaatcttctgattctgtagtagatgaggttcaccata 1451
DB 225 GTGCTGCCACCATGCTAGTAAATTTTGTATTATTTAGCACAGATGGGTTTCACCAT 284
QY 1452 ttgagccggtggtcttgaactctgaacctcaggtgataccaccactgaagctcttaa 1511
DB 285 TTGCTGAGGCTGTCTGGAATCTCTAATCATGTATCATCCCGTCTCAGCTCCCAAA 344
QY 1512 gtgctgattacaggaagctacagcgcccgccgaaggtcagtgcttaataagaa 1571
DB 345 GTGCTGGGATTACAGCGGTAGCCACCGCTGCTGTCAGGGGTATGTTTATAGAA 404
QY 1572 taacttga 1580
DB 405 TAATCTGCA 413

Mon Dec 4-08:51:43 2000

us-09-227-881-34.rst

Page 10

Db 65 CTTGCTCTGCTTTGCTA 48

Search completed: December 3, 2000, 10:15:41
job time: 14019 sec